

**LISTING OF CLAIMS**

Please amend the claims as indicated, with the understanding that they have been labeled pursuant to a request by the Office for convenience in examination. The amendment or cancellation of a claim or reference to a claim as "currently amended", "canceled" or "withdrawn" is not an admission that the claim was amended or canceled for any reason related to patentability. The claim listing below replaces all prior versions and listings of claims in this application.

1. (Original) An isolated MNTF associated polynucleotide selected from the group consisting of a sequence comprising SEQ ID NO:1; a sequence comprising SEQ ID NO:2; and complements of the preceding.
2. (Original) The isolated polynucleotide of claim 1 comprising a fragment of SEQ ID NO:1, said fragment comprising i) a 5' terminus selected from residues 1-1849 of SEQ ID NO:1, and ii) at least ten consecutive nucleic acid residues of SEQ ID NO:1 including the 5' terminus and a 3' terminus, wherein the 3' terminus of said fragment is selected from residues 10-1859 of SEQ ID NO:1.
3. (Original) An isolated polynucleotide comprising a fragment of SEQ ID NO:1, provided that the nucleotide sequence of said fragment contains at least one nucleotide selected from any of the following: residues 1-582; residues 758-765; residues 886-892; residues 1104-1108; residues 1126-1129; residues 1165-1173; residues 1174-1182; residues 1183-1192; residues 1192-1198; residues 1224-1225; residue 1267; residue 1289; residues 1321-1323; residues 1334-1336; residues 1339-1341; residues 1346-1349; residues 1364-1372; residues 1403-1406; residues 1450-1452; residues 1467-1473, and residues 1474-1859 of SEQ ID NO:1.

4. (Original) The isolated polynucleotide of claim 1 comprising a fragment of SEQ ID NO:1 selected from the group consisting of:
- a) SEQ ID NO:3;
  - b) SEQ ID NO:5;
  - c) SEQ ID NO:6; and
  - d) SEQ ID NO:10.
5. (Original) The isolated polynucleotide of claim 1 comprising a fragment having a nucleic acid sequence fully complementary SEQ ID NO:1 that is selected from the group consisting of:
- a) SEQ ID NO:4;
  - b) SEQ ID NO:7;
  - c) SEQ ID NO:8;
  - d) SEQ ID NO:11; and
  - e) SEQ ID NO:12.
6. (Original) The isolated polynucleotide fragment of claim 3 comprising at least one open reading frame.
7. (Original) The isolated polynucleotide of claim 6 wherein the at least one open reading frame encodes a polypeptide selected from the group consisting of:
- a) SEQ ID NO:13;
  - b) SEQ ID NO:14;
  - c) SEQ ID NO:15;
  - d) SEQ ID NO:16;
  - e) SEQ ID NO:17;
  - f) SEQ ID NO:18;
  - g) SEQ ID NO:19;
  - h) SEQ ID NO:20;
  - i) SEQ ID NO:21;
  - a) SEQ ID NO:22;

- b) SEQ ID NO:23;
- c) SEQ ID NO:24;
- d) SEQ ID NO:25;
- e) SEQ ID NO:26;
- f) SEQ ID NO:27;
- g) SEQ ID NO:28;
- h) SEQ ID NO:29;
- i) SEQ ID NO:30;
- j) SEQ ID NO 31; and
- k) SEQ ID NO: 32.

8. (Original) A composition comprising a first polynucleotide and a second polynucleotide according to claim 7, wherein the first polynucleotide contains an open reading frame encoding SEQ ID NO:29.

9. (Original) The isolated polynucleotide of claim 3, said fragment of SEQ ID NO:2 comprising at least one putative MNTF promoter sequence and at least one open reading frame.

10. (Original) The isolated polynucleotide of claim 9 wherein said putative MNTF promoter sequence is selected from the group consisting of:

- a) residues 862-911 of SEQ ID NO:2; and
- b) residues 2315-2364 of SEQ ID NO:2.

11. (Original) The isolated polynucleotide of claim 10 wherein said fragment of SEQ ID NO:2 includes a potential transcription start sequence comprising residues 2501-4359 of SEQ ID NO:2.

12. (Original) The isolated polynucleotide of claim 9 wherein the at least one open reading frame encodes a polypeptide selected from the group consisting of:

- a) SEQ ID NO:13;

- b) SEQ ID NO:14;
- c) SEQ ID NO:15;
- d) SEQ ID NO:16;
- e) SEQ ID NO:17;
- f) SEQ ID NO:18;
- g) SEQ ID NO:19;
- h) SEQ ID NO:20;
- i) SEQ ID NO:21;
- j) SEQ ID NO:22;
- k) SEQ ID NO:23;
- l) SEQ ID NO:24;
- m) SEQ ID NO:25;
- n) SEQ ID NO:26;
- o) SEQ ID NO:27;
- p) SEQ ID NO:28;
- q) SEQ ID NO:29;
- r) SEQ ID NO:30;
- s) SEQ ID NO 31; and
- t) SEQ ID NO: 32.

13. (Withdrawn) An isolated MNTF associated polypeptide encoded by an open reading frame of SEQ ID NO:1.

14. (Withdrawn) A fusion protein comprising an MNTF associated polypeptide encoded by an open reading frame of SEQ ID NO:1 linked to a heterologous protein.

15. (Original) An expression vector operably linked to the isolated polynucleotide according to claim 1, wherein at least one open reading frame is operably linked to a control sequence compatible with a desired host vector.

16. (Original) An isolated host cell transformed with the expression vector of claim 15.
17. (Withdrawn) A method for determining the presence of a MNTF associated polynucleotide in a medium comprising the steps of:
  - contacting the medium, which may contain an MNTF associated nucleic acid sequence, with a synthesized and isolated oligonucleotide which under preselected hybridization conditions hybridizes with said MNTF associated nucleic acid sequence, but does not hybridize with nucleic acid sequences other than said MNTF associated nucleic acid sequence, in said medium; and
  - detecting, under said preselected hybridization conditions, the presence of said MNTF associated nucleic acid sequence.
18. (Withdrawn) A method of comparing the relative abundance of MNTF associated expression products in different samples comprising:
  - obtaining a first sample and a second sample, wherein the first sample differs from the second sample;
  - detecting a MNTF related expression product for the first sample and the second sample;
  - and comparing the relative abundance of the MNTF associated expression products of the first and second samples.
19. (Withdrawn) The method of claim 18, wherein MNTF RNA is the expression product.
20. (Withdrawn) The method of claim 18, wherein an MNTF associated polypeptide is the expression product.
21. (Withdrawn) The method of claim 18, wherein an MNTF associated polypeptide encoded by an open reading frame of SEQ ID NO:1 is the expression product.
22. (Withdrawn) The method of claim 18, wherein a polypeptide having at least SEQ ID NO. 29 is the expression product.

23. (Withdrawn) The method of claim 18, wherein the comparison includes a step comprising hybridization with a nucleic acid probe complementary to the RNA.
24. (Original) A panel for use in hybridization assays comprising two or more polynucleotides according to claim 1 stably associated with the surface of a solid support.
25. (Original) An isolated polynucleotide comprising a fragment of SEQ ID NO:1 or SEQ ID NO:2, provided that the nucleotide sequence of said fragment does not entirely correspond to SEQ ID NO:2 in U.S. Pat. No. 6,309,877.
26. (Original) An isolated polynucleotide comprising a fragment of SEQ ID NO:1 or SEQ ID NO:2, provided that the nucleotide sequence of said fragment does not entirely correspond to SEQ ID NO:5 in U.S. Pat. No. 6,309,877.
27. (New) The isolated polynucleotide of claim 1 consisting of SEQ ID NO:1.